

IncK plasmid-mediated tetracycline resistance in *Edwardsiella ictaluri* isolates from diseased freshwater catfish in Vietnam

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22 ABSTRACT

23 Eight tetracycline resistant *Edwardsiella ictaluri* isolates obtained from diseased freshwater catfish
24 (*Pangasianodon hypophthalmus*) in Vietnam, and showing different resistance phenotypes to other
25 antimicrobial agents, were studied. The *tet* genes were determined using PCR. Conjugation
26 experiments were performed to assess transferability of the tetracycline resistance determinant and the
27 size and incompatibility group (Inc) of each *tet*-carrying plasmid were determined. PCR and
28 sequencing were used for characterization of the co-transferred resistance genes. A *tetA* gene was
29 demonstrated in the *E. ictaluri* isolates and for all of them, *E. coli* transconjugants were obtained. All
30 transconjugants contained high-molecular weight *tetA*-carrying plasmids (~140 kb) belonging to the
31 *incK* group, as was shown with the PCR-based replicon typing method. The *strA-strB*, *dhfr1* and *sul 2*
32 genes were detected on the *tetA*-carrying plasmids of the transconjugants showing resistance to
33 streptomycin, trimethoprim and sulfonamides, respectively. The *dhfr1* gene was found to be located in
34 a class 1 integron as determined by PCR and sequencing. Interestingly, the 3' CS region of class 1
35 integrons was not detected by PCR. This study shows the presence of *incK* plasmid-mediated
36 tetracycline resistance among *E. ictaluri* isolates from diseased freshwater catfish in Vietnam.

37

1. Introduction

Industrial aquaculture is a rapidly growing industry in many developed and developing countries, as Vietnam, where the freshwater catfish *Pangasianodon hypophthalmus* has grown into a global giant faster than any other aquaculture species in history. This indigenous fish species is high in demand from global consumers. With the rapid expansion and intensification of the freshwater industry, infectious diseases often break out. Bacillary necrosis caused by *Edwardsiella ictaluri*, is responsible for serious economical damage in Vietnamese catfish farms and for control of this disease, antimicrobial agents are often used both prophylactically and therapeutically (Crumlish et al., 2002; Ferguson et al., 2001). This may favor the spread of antimicrobial resistance genes in fish-associated and environmental aquatic bacteria.

In a recent study, acquired resistance to oxytetracycline was demonstrated in 52 of 64 Vietnamese *E. ictaluri* isolates tested and the majority of these isolates also showed acquired resistance to other antimicrobial agents, including streptomycin, sulphonamides and trimethoprim (Dung et al., 2008). Different mechanisms of resistance to tetracyclines have been described with ribosomal protection, efflux and enzymatic inactivation of the antibiotic as major modes of action. Most tetracycline resistant bacteria carry one or more of the 40 different tetracycline resistance genes described so far (Brown et al., 2008; Chopra et al., 2001; Robert, 2005).

The aim of the present study was to determine the genetic determinants of tetracycline resistance among *E. ictaluri* isolates from Vietnamese freshwater catfish and to assess its transferability. Genes encoding resistance to other antimicrobial agents which were co-transferred during conjugation experiments were also characterized.

59 **2 Materials and methods**

60 *2.1 Bacterial isolates and determination of tet genes*

61 Eight of the 52 tetracycline resistant *E. ictaluri* isolates obtained during a previous study and showing
62 the three most prevalent antimicrobial resistance phenotypes (Dung et al., 2008), were selected (Table
63 1). All selected isolates were obtained from the kidney of diseased catfish (*Pangasianodon*
64 *hypophthalmus*) during different outbreaks of bacillary necrosis in Vietnam. For the determination of
65 the *tet* genes, PCR was performed (Cauwerts et al., 2006; Jun et al., 2004). Total DNA (genomic and
66 plasmid DNA) and PCR mixtures were prepared as described previously (Baele et al., 2000; Martel et
67 al., 2001).

68
69 *2.2 Conjugation experiments*

70 Conjugation experiments were carried out in Luria Broth medium with *E. coli* J5, resistant to
71 rifampicin, used as the recipient strain. Tests were performed overnight at 37°C with a donor/recipient
72 ratio of 0.2. Transconjugants were selected on MacConkey agar plates (Oxoid LTD, Basingstoke,
73 Hampshire, England) supplemented with tetracycline (25 mg/L) and rifampicin (250 mg/L) (Bertrand
74 et al., 2006). The transfer frequency was estimated by dividing the number of transconjugants per
75 milliliter by the number of recipients per milliliter.

76
77 *2.3 Antimicrobial susceptibility testing*

78 The antimicrobial susceptibility of the *E. coli* transconjugants was determined by the Kirby Bauer disk
79 diffusion test (Neo-sensitabs, Rosco Diagnostica, Taastrup, Denmark) as described previously

80 (document M31-A3) (Table 1) (NCCLS, 2008; Smet et al., 2008). Clinical Laboratory Standards
81 Institute (CLSI) guidelines were followed for inoculum standardization, medium and incubation
82 conditions, and internal quality control organisms (*E. coli* ATCC 25922).

83

84 *2.4 Plasmid analysis*

85 Plasmid profiles were determined for the *E. ictaluri* isolates and their *E. coli* transconjugants (Kado and
86 Liu, 1981). The molecular size of each *tet*-carrying plasmid was estimated by using a BAC Tracker
87 Supercoiled DNA ladder (Epicentre Biotechnologies, Madison, Wisconsin). Plasmid DNA of the *E.*
88 *coli* transconjugants was obtained as described by Takahashi and Nagano (1984). The incompatibility
89 (Inc) group of each *tet*-carrying plasmid was determined by the PCR-based replicon typing (PBRT)
90 method (Carattoli et al., 2005).

91

92 *2.5 Molecular characterization of co-transferred resistance genes*

93 The characterization of the co-transferred resistance determinants on the *tet*-carrying plasmids were
94 performed by PCR and sequencing on plasmid DNA of the *E. coli* transconjugants as described in
95 previous reports (Bertrand et al., 2006; Costa et al., 2008; Huys et al., 2005; Schmidt et al., 2007;
96 Zhang et al., 2004).

97

98 **3. Results**

99 PCR, with primers specific for different tetracycline resistance genes, demonstrated the presence of a
100 *tetA* gene among all selected isolates.

101 *E. coli* transconjugants were obtained for all isolates. The characteristics of the *E. ictaluri* strains and
102 their *tetA*-carrying plasmids are shown in Table 1. Transfer frequency was approximately 2.54×10^{-6} .
103 Antimicrobial susceptibility testing of the *E. coli* transconjugants revealed that all other resistance
104 determinants, with the exception of flumequine resistance, were cotransferred with the tetracycline
105 resistance determinant. Plasmid analysis showed a strong band of approximately 140 kb indicating the
106 presence of a high-molecular weight *tetA*-carrying plasmid for all transconjugants (data not shown).
107 The PBRT method applied on plasmid DNA of the transconjugants showed that all plasmids carrying
108 the *tetA* gene belonged to the *incK* group.

109 Characterization of the co-transferred resistance determinants was performed by PCR on plasmid DNA
110 with primers specific for trimethoprim, sulfonamide and streptomycin resistance genes. The *strA-strB*
111 genes were detected on the *tetA*-carrying plasmids of the transconjugants that showed resistance to
112 streptomycin. The *aadA* gene, another streptomycin resistance determinant, was not found. The *dhfr1*
113 and *sul2* genes were found on the *tetA*-carrying plasmids of the transconjugants showing resistance to
114 trimethoprim and sulphonamides, respectively. Often the trimethoprim resistance determinant is
115 located in an integron. Therefore, PCR with primers specific for the class 1 (*intI1*) and class 2 (*intI2*)
116 integrase was performed (Zhang et al., 2004)). Only the *intI1* gene was identified on all *tetA*-carrying
117 plasmids indicating the presence of class 1 integrons. Characterization of the variable region of class 1
118 integrons by PCR and DNA sequencing revealed a 500 bp gene cassette, *dhfr1*. Class 1 integrons
119 normally possess a 5' conserved segment (5'CS) and a 3' conserved segment (3'CS) separated by a
120 variable region. However, the 3'CS, containing the *qacΔE1* and *sul1* genes and an open reading frame
121 *orf5*, was not detected by PCR for all class 1 integrons located on the *tetA*-carrying plasmids.

122 4. Discussion

123 Recently, public health agencies have raised a worldwide concern about the impact of antimicrobial use
124 in the aquaculture environment (Huys et al., 2005). The emergence of antimicrobial resistance among
125 fish pathogens undermines the effectiveness of antimicrobial therapy in aquaculture. It also increases
126 the possibilities for transfer of resistance determinants from aquatic bacteria to bacteria of terrestrial
127 animals and human beings, including pathogens (Costa et al., 2008; Huys et al., 2005; Schmidt et al.,
128 2001; Sun et al., 2009). Therefore, the exchange of antimicrobial resistance genes between bacteria in
129 the aquaculture environment is of great concern. Very few information is available about plasmid-
130 borne resistance genes among *E. ictaluri* isolates (Welch et al., 2009). Therefore, the genetic
131 determinants of tetracycline resistance and its transferability were studied.

132 A *tetA* gene was demonstrated in the *E. ictaluri* isolates. This gene, as well as other tetracycline
133 resistance determinants, has also been described in other fish pathogens (Aoki et al., 1987; Crumlish et
134 al., 2002; Miranda et al., 2003; Schmidt et al., 2001; Sun et al., 2009). Several studies have investigated
135 the genetic support of the *tetA* gene and found a Tn1721-like transposon to be involved in its mobility
136 (Ojo et al., 2003; Rhodes et al., 2000; Sorum et al., 2003). The *tetA* gene present in our isolates may be
137 carried by a Tn1721-like transposon, but this needs further investigation.

138 All transconjugants contained high-molecular weight *tetA*-carrying plasmids (~140 kb) belonging to the
139 IncK group, as was shown with the PBRT method. To our knowledge, this is the first description of the
140 *tetA* gene on *incK* plasmids in *E. ictaluri*. In a recent study an IncA/C plasmid, containing genes
141 encoding tetracycline resistance, was demonstrated in an *Edwardsiella ictaluri* strain (Welch et al.,
142 2009). The *tetA* gene was also found to be located on a smaller plasmid in an *Aeromonas salmonicida*

143 isolate (Schmidt et al., 2001; Sørum et al., 2003). These findings might indicate that this gene is
144 circulating among different plasmids. Further characterization of our *incK* plasmids and comparison
145 with other plasmids, containing tetracycline resistance determinants, may help to explain the spread of
146 this gene among several plasmids.

147 The linked *strA-strB* gene pair was detected on the *tetA*-carrying plasmids of the transconjugants
148 showing resistance to streptomycin. This gene pair is widely disseminated among diverse gram-
149 negative bacteria and has also been detected in other bacteria isolated from farmed fish (L'Abée-Lund
150 and Sørum, 2000; Sunde and Norström, 2005). A study in Norway characterized a small plasmid from
151 the fish pathogen *Aeromonas salmonicida* and showed that the *strA-strB* genes were carried by a
152 Tn5393-like transposon (L'Abée-Lund and Sørum, 2000). The genetic support of the linked *strA-strB*
153 gene pair on our *tetA*-carrying plasmids remains unknown and needs further investigation.

154 The *dhfr1* gene, encoding resistance to trimethoprim, was found to be located in a class 1 integron as
155 determined by PCR and sequencing. This gene cassette was also found in class 1 integrons associated
156 with plasmids in clinical *Aeromonas salmonicida* isolates (Schmidt et al., 2001). Interestingly, the 3'CS
157 was not detected in our class 1 integrons by PCR. This may indicate that the priming site in the 3'CS is
158 missing. The presence of these 3'CS-lacking integrons has also been reported in bacteria from an
159 aquatic environment and at low frequencies in *E. coli* recovered from humans and animals (Rosser and
160 Young, 1999; Saenz et al., 2004; Vinué et al., 2008).

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163

164 **5. Conclusion**

165 This study shows the presence of *incK* plasmids carrying tetracycline, streptomycin, trimethoprim and
166 sulphonamide resistance genes among *E. ictaluri* isolates from diseased freshwater catfish. It further
167 strengthens the need for prudent use of antimicrobial agents in catfish production.

168

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174

175 **References**

- 176 Aoki, T., Takahashi, A., 1987. Class D tetracycline resistance determinants of R plasmids from the fish
177 pathogens *Aeromonas hydrophila*, *Edwardsiella tarda* and *Pasteurella piscicida*.
178 Antimicrob. Agents Chemother. 31, 1278–1280
- 179 Baele, M., Baele, P., Vaneechoutte, M., Storms, V., Butaye, P., Devriese, L.A., Verschraegen, G.,
180 Gillis M., Haesebrouck, F., 2000. Application of tDNA-PCR for the identification of
181 *Enterococcus* species. J. Clin. Microbiol. 38, 4201-4207.
- 182 Bertrand, S., Weill, F.X., Cloeckaert, A., Vrints, M., Mairiaux, E., Praud, K., Dierick, K., Wildemaue,
183 C., Godard, C., Butaye, P., Imberechts, H., Grimont, P.A., Collard, J.M., 2006. Clonal
184 emergence of extended-spectrum beta-lactamase (CTX-M-2)-producing *Salmonella*

185 *enterica* serovar *Virchow* isolates with reduced susceptibilities to ciprofloxacin among
 186 poultry and humans in Belgium and France (2000 to 2003). J. Clin. Microb. 44, 2897-
 187 2903.

188 Brown, M.G., Mitchell, E.H., Balkwill, D.L., 2008. Tet 42, a novel tetracycline resistance determinant
 189 isolated from deep terrestrial subsurface bacteria. Antimicrob. Agents Chemother. 52,
 190 4518-4521.

191 Carattoli, A., Bertini, A., Villa, L., Falbo, V., Hopkins, K.L., Threlfall, E.J., 2005. Identification of
 192 plasmids by PCR-based replicon typing. J. Microbiol. Methods 63, 219-228.

193 Cauwerts, K., Pasmans, F., Devriese, L.A., Haesebrouck, F., Decostere A., 2006. Cloacal *Lactobacillus*
 194 isolates from broilers often display resistance toward tetracycline antibiotics. Microb.
 195 Drug Res. 2, 284-288.

196 Chopra, I., Roberts, M., 2001 Tetracycline antibiotics: mode of action, applications, molecular biology,
 197 and epidemiology of bacterial resistance. Microb. Mol. Biol. Rev. 65, 232-260.

198 Costa, D., Poeta, P., Saenz, Y., Vinué, L., Coelho, A.C., Matos, M., Bezares, B.R., Rodrigues, J.,
 199 Torres, C., 2008. Mechanisms of Antibiotic resistance in *Escherichia coli* isolates
 200 recovered from wild animals. Microb. Drug Res. 14, 71-77.

201 Crumlish, M., Dung, T.T., Turnbull, J.F., Ngoc, N.T.N., Ferguson, H.W., 2002. Identification of
 202 *Edwardsiella ictaluri* from diseased freshwater catfish, *Pangasius hypophthalmus*
 203 (Sauvage), cultured in the Mekong Delta, Vietnam. J. Fish Dis. 25, 733-736.

204 Dung, T.T., Haesebrouck, F., Tuan, N.A., Sorgeloos, P., Baele, M., Decostere, A., 2008. Antimicrobial
205 Susceptibility Pattern of *Edwardsiella ictaluri* isolates from natural outbreaks of Bacillary
206 Necrosis of *Pangasianodon hypophthalmus* in Vietnam. Microb. Drug Res. 14, 311-316.

207 Ferguson, H.W., Turnbull, J.F., Shinn, A., Thompson, K., Dung, T.T., Crumlish, M., 2001. Bacillary
208 necrosis in farmed *Pangasius hypophthalmus* (Sauvage) from the Mekong Delta,
209 Vietnam. J. Fish Dis. 24, 509-513.

210 Huys, G., Cnockaert, M., Vaneechoutte, M., Woodford, N., Nemec, A., Dijkshoorn, L., Swings, J.,
211 2005. Distribution of tetracycline resistance genes in genotypically related and unrelated
212 multiresistant *Acinetobacter baumannii* strains from different European hospitals. Res.
213 Microb. 156, 348-55.

214 Jun, L.J., Jeong, J.B., Huh, M.D., Chung, J.K., Choi, D.I., Jeong, H.D., 2004. Detection of
215 tetracycline-resistance determinants by multiplex polymerase chain reaction in
216 *Edwardsiella tarda* isolated from fish farms in Korea. Aquaculture 240, 89-100.

217 Kado, C.I., Liu, S.T., 1981. Rapid procedure for the detection of large and small plasmids. J. Bacteriol.
218 145, 1365-1373.

219 L'Abée-Lund, T., Sørum, H., 2000. Functional Tn5393-like transposon in the R plasmid pRAS2 from
220 the fish pathogen *Aeromonas salmonicida* subspecies *salmonicida* isolated in Norway.
221 Appl. Environm. Microbiol. 66, 5533-5535.

222 Martel, A., Baele, M., Devriese, L.A., Goossens, H., Wisselink, H.J., Decostere, A., Haesebrouck,
223 F., 2001. Prevalence and mechanism of resistance against macrolides and lincosamides
224 in *Streptococcus suis* isolates. Vet. Microb. 83, 287-297.

225 Miranda, C.D., Kehrenberg, C., Ulep, C., Schwarz, S., Roberts, M.C.. 2003. Diversity of tetracycline
 226 resistance genes in bacteria from Chilean salmon farms. Antimicrob. Agents Chemother.
 227 47, 883-888.

228 National Committee for Clinical Laboratory Standards. Performance standards for antimicrobial disk
 229 and dilution susceptibility tests for bacteria isolated from animals-third edition: approved
 230 standard M31-A3. CLSI, Wayne, PA, USA, 2008.

231 Ojo, K.K., Kehrenberg C., Odelola, H.A., 2003. Structural analysis of the tetracycline resistance gene
 232 region of a small multiresistance plasmid from uropathogenic *Escherichia coli* isolated in
 233 Nigeria. Aquaculture 52, 1043-1044.

234 Rhodes, G., Huys, G., Swings, J., McGann, P., Hiney, M., Smith, P., Pickup, R.W., 2000. Distribution
 235 of oxytetracycline resistance plasmids between aeromonads in hospital and aquaculture
 236 environments: implication of Tn1721 in dissemination of the tetracycline resistance
 237 determinant Tet A. Appl. Environ. Microbiol. 66, 3883-3890.

238 Robert, M.C., 2005 Update on acquired tetracycline resistance genes. FEMS Microb. Lett. 245, 195-
 239 203.

240 Rosser, S.J., Young, H.K., 1999. Identification and characterization of class 1 integrons in bacteria
 241 from an aquatic environment. J. Antimicrob. Chemother. 44, 11-18.

242 Sáenz, Y., Briñas, L., Domínguez, E., Ruiz, J., Zarazaga, M., Vila, J., Torres, C., 2004. Mechanisms of
 243 resistance in multiple-antibiotic-resistant *Escherichia coli* strains of human, animal, and
 244 food origins. Antimicrob. Agents Chemother. 48: 3995-4001.

245 Schmidt A.S., Bruum, M.S., Dalsgaard, I., Larsen, J.L., 2001. Characterization of class 1 integrons
 246 associated with R-plasmids in clinical *Aeromonas salmonicida* isolates from various
 247 geographical areas. J. Antimicrob. Chemother. 47, 735-743.

248 Smet, A., Martel, A., Persoons, D., Dewulf, J., Heyndrickx, M., Catry, B., Herman, L., Haesebrouck,
 249 F., Butaye, P., 2008. Diversity of extended-spectrum β -lactamases and class C β -
 250 lactamases among cloacal *Escherichia coli* in Belgian broiler farms. Antimicrob. Agents
 251 Chemother. 52, 1238-1243.

252 Sørum, H., L'Abée-Lund, T.M., Solberg, A., Wold, A., 2003. Integron-containing IncU R plasmids
 253 pRAS1 and pAr-32 from the fish pathogen *Aeromonas salmonicida*. Antimicrob. Agents
 254 Chemother. 47, 1285-1290.

255 Sun, K., Wang, H.L., Zhang, M., Xiao, Z.Z., Sun, L., 2009. Genetic mechanisms of multi-antimicrobial
 256 resistance in a pathogenic *Edwardsiella tarda* strain. Aquaculture 289, 134-139.

257 Sunde, M., Norström, M., 2005. The genetic background for streptomycin resistance in *Escherichia*
 258 *coli* influences the distribution of MICs. J. Antimicrob. Chemother. 56, 87-90.

259 Takahashi, S., Nagano, Y., 1984. Rapid procedure for isolation of plasmid DNA and application to
 260 epidemiological analysis. J. Clin. Microbiol. 20, 608-613.

261 Vinué, L., Sáenz, Y., Somalo, S., Escudero, E., Moreno, M.A., Ruiz-Larrea, F., Torres, C., 2008.
 262 Prevalence and diversity of integrons and associated resistance genes in faecal
 263 *Escherichia coli* isolates of healthy humans in Spain. J. Antimicrob. Chemother. 62, 934-
 264 937.

265 Welch, T.J., Evenhuis, J., White, D., McDermott, P.F., Harbottle, H., Miller, R.A., Griffin, M., Wise,
266 D., 2009. IncA/C plasmid-mediated florfenicol resistance in catfish pathogen
267 *Edwardsiella ictaluri*. Antimicrob. Agents Chemother. 53:845-846.

268 Zhang, H., Shi, L., Guo, S., Zhang, X., Yamaski, S., Miyoshi, S., Shinoda, S., 2004. Identification and
269 characterization of class 1 integron resistance gene cassettes among *Salmonella* strains
270 isolated from healthy humans in China. Microb. Immunol. 48, 639-645.

271

272 **Table 1**

273 Characteristics of the *E. ictaluri* strains and the *tetA*-carrying plasmids analysed in this study

274

<i>Isolate number</i>	Year of isolation	Antimicrobial resistance ^a (parental strains)	co-transferred resistance	Antimicrobial resistance genes on the plasmid	Transfer frequency
E18	2002	TET, TMP	TMP	<i>tetA, dhfr1</i>	1.35 X 10 ⁻⁶
E29	2002	TET, TMP	TMP	<i>tetA, dhfr1</i>	2.05 X10 ⁻⁶
LO2	2002	TET, TMP, SULF, STR	TMP, SULF, STR	<i>tetA, dhfr1, sul2, strA-strB</i>	3.65 X 10 ⁻⁶
QO2	2002	TET, TMP, SULF, STR	TMP, SULF, STR	<i>tetA, dhfr1, sul2, strA-strB</i>	1.27 X 10 ⁻⁵
198	2002	TET, TMP, SULF, STR, Flum	TMP, SULF, STR	<i>tetA, dhfr1, sul2, strA-strB</i>	3.42 X 10 ⁻⁶
192	2002	TET, TMP, SULF, STR, Flum	TMP, SULF, STR	<i>tetA, dhfr1, sul2, strA-strB</i>	3.65 X 10 ⁻⁷
E136	2005	TET, TMP, SULF, STR	TMP, SULF, STR	<i>tetA, dhfr1, sul2, strA-strB</i>	1.03 X 10 ⁻⁷
E137	2005	TET, TMP, SULF, STR	TMP, SULF, STR	<i>tetA, dhfr1, sul2, strA-strB</i>	3.90 X 10 ⁻⁶

275

276 ^a Antimicrobial drugs used were the following: flumequine (Flum), tetracycline (TET), trimethoprim (TMP), streptomycin (STR), sulfonamides

277 (SULF)